## SEQUENCE LISTING

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<110> TREUHEIT, MICHAEL O'CONNER, SHEILA KOSKY, ANDREW
<120> PROCESS FOR CORRECTION OF A DISULFIDE MISFOLD IN Fc MOLECULES
<130> A-584
<140> To Be Assigned <141> 2000-11-09
<150> 60/165,188 <151> 1999-11-12
<160> 2
<170> PatentIn version 3.0
<210> 1 <211> 684 <212> DNA <213> Homo sapiens
<220> <221> CDS <222> (1)(684)
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atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc  Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser  35 40 45
cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac gtg gag His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu 50 55 60
gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr 65 70 75 80
tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn 85 90 95
ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc 336 Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro 100 105 110
atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga gaa cca cag Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln 115 120 125
gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag aac cag gtc 432 Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val

	130					135					140						
agc Ser 145	ctg Leu	acc Thr	tgc Cys	ctg Leu	gtc Val 150	aaa Lys	ggc Gly	ttc Phe	tat Tyr	ccc Pro 155	agc Ser	gac Asp	atc Ile	gcc Ala	gtg Val 160	48	80
gag Glu	tgg Trp	gag Glu	agc Ser	aat Asn 165	ggg	cag Gln	ccg Pro	gag Glu	aac Asn 170	aac Asn	tac Tyr	aag Lys	acc Thr	acg Thr 175	cct Pro	52	28
ccc Pro	gtg Val	ctg Leu	gac Asp 180	tcc Ser	gac Asp	ggc Gly	tcc Ser	ttc Phe 185	ttc Phe	ctc Leu	tac Tyr	agc Ser	aag Lys 190	ctc Leu	acc Thr	51	76
gtg Val	gac Asp	aag Lys 195	agc Ser	agg Arg	tgg Trp	cag Gln	cag Gln 200	ggg Gly	aac Asn	gtc Val	ttc Phe	tca Ser 205	tgc Cys	tcc Ser	gtg Val	62	24
atg Met	cat His 210	gag Glu	gct Ala	ctg Leu	cac His	aac Asn 215	cac His	tac Tyr	acg Thr	cag Gln	aag Lys 220	agc Ser	ctc Leu	tcc Ser	ctg Leu	67	72
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Met 1		Lys		5					10					15			
Met 1 Gly	Asp	Lys Pro	Ser 20	5 Val	Phe	Leu	Phe	Pro 25	10 Pro	Lys	Pro	Lys	Asp 30	15 Thr	Leu		
Met 1 Gly Met	Asp Gly	Lys Pro Ser 35	Ser 20 Arg	5 Val Thr	Phe Pro	Leu Glu	Phe Val 40	Pro 25 Thr	10 Pro Cys	Lys Val	Pro Val	Lys Val 45	Asp 30	15 Thr Val	Leu Ser		
Met 1 Gly Met His	Asp Gly Ile Glu	Lys Pro Ser 35	Ser 20 Arg Pro	5 Val Thr	Phe Pro Val	Leu Glu Lys 55	Phe Val 40 Phe	Pro 25 Thr	10 Pro Cys Trp	Lys Val Tyr	Pro Val Val 60	Lys Val 45 Asp	Asp 30 Asp Gly	15 Thr Val Val	Leu Ser Glu		
Met 1 Gly Met His	Asp Gly Ile Glu 50	Lys Pro Ser 35 Asp	Ser 20 Arg Pro	Val Thr Glu Lys	Phe Pro Val	Leu Glu Lys 55 Lys	Phe Val 40 Phe	Pro 25 Thr Asn	10 Pro Cys Trp Glu	Lys Val Tyr Glu 75	Pro Val Val 60	Lys Val 45 Asp	Asp 30 Asp Gly Asn	15 Thr Val Val Ser	Leu Ser Glu Thr		
Met  Gly  Met  His  Val 65	Asp Gly Ile Glu 50	Lys Pro Ser 35 Asp Asn	Ser 20 Arg Pro Ala Val	Val Thr Glu Lys Ser 85	Phe Pro Val Thr 70 Val	Leu Glu Lys 55 Lys	Phe Val 40 Phe Pro	Pro 25 Thr Asn Arg	10 Pro Cys Trp Glu Leu 90	Lys Val Tyr Glu 75	Pro Val Val 60 Gln	Lys Val 45 Asp Tyr	Asp 30 Asp Gly Asn	15 Thr Val Val Ser Leu 95	Leu Ser Glu Thr 80		

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Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val 130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val 145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro 165 170 175

Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val 195 200 205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu 210 215 220

Ser Pro Gly Lys 225